Amendments to the Claims

The listing of claims will replace all prior versions, and listings of claims in the application.

1-214. (Canceled)

215. (Previously presented) A method to prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof a composition comprising a carrier, (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradecenyloxy)-1-propanaminium bromide (GAP-DMORIE), a co-lipid and an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 97% identical to amino acids 199 to 764 of SEQ ID NO:4,

wherein said composition elicits an immune response to said polypeptide;

and wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

216. (Previously presented) The method of claim 215, wherein the amino acids of said polypeptide corresponding to amino acids 342 and 343 of SEQ ID NO:4 have been deleted.

217. (Previously presented) The method of claim 215, wherein said polypeptide comprises amino acids 199 to 764 of SEQ ID NO:4.

218. (Previously presented) The method of claim 215, wherein said nucleic acid fragment encodes a polypeptide at least 97% identical to amino acids 30 to 764 of SEQ ID NO:4.

219. (Previously presented) The method of claim 217, wherein said polypeptide comprises amino acids 30 to 764 of SEQ ID NO:4.

220. (Previously presented) The method of claim 218, wherein the amino acids of said polypeptide corresponding to amino acids 192 to 197 of SEQ ID NO:4 have been deleted.

221. (Previously presented) The method of claim 220, wherein said polypeptide is SEQ ID NO:8.

222. (Previously presented) The method of claim 215, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

223. (Previously presented) The method of claim 222, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

224. (Previously presented) The method of claim 223, wherein said heterologous polypeptide is a secretory signal peptide.

225. (Previously presented) The method of claim 224, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

226. (Previously presented) The method of claim 215, wherein said co-lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

227. (Previously presented) The method of claim 226, wherein said co-lipid is DPyPE.

228. (Previously presented) The method of claim 227, wherein said GAP-DMORIE and DPyPE are in a 1:1 molar ratio.

229. (Previously presented) The method of claim 228, wherein said polypeptide is SEQ ID NO:8.

230. (Previously presented) The method of claim 215, wherein said composition further comprises a nucleic acid molecule which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of: amino acids 30 to 764 of SEQ ID NO:4, SEQ ID NO:6; SEQ ID NO:8; and a combination of two or more of said amino acid sequences.

231. (Currently amended) A method to ~~treat~~ reduce the severity of anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof a composition comprising a carrier, (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradecenyloxy)-1-propanaminium bromide (GAP-DMORIE), a co-lipid and an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 97% identical to amino acids 199 to 764 of SEQ ID NO:4,

wherein said composition elicits an immune response to said polypeptide;

and wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said

leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

232. (Previously presented) The method of claim 231, wherein the amino acids of said polypeptide corresponding to amino acids 342 and 343 of SEQ ID NO:4 have been deleted.

233. (Previously presented) The method of claim 231, wherein said polypeptide comprises amino acids 199 to 764 of SEQ ID NO:4.

234. (Previously presented) The method of claim 231, wherein said nucleic acid fragment encodes a polypeptide at least 97% identical to amino acids 30 to 764 of SEQ ID NO:4.

235. (Previously presented) The method of claim 233, wherein said polypeptide comprises amino acids 30 to 764 of SEQ ID NO:4.

236. (Previously presented) The method of claim 234, wherein the amino acids of said polypeptide corresponding to amino acids 192 to 197 of SEQ ID NO:4 have been deleted.

237. (Previously presented) The method of claim 236, wherein said polypeptide is SEQ ID NO:8.

238. (Previously presented) The method of claim 231, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

239. (Previously presented) The method of claim 238, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

240. (Previously presented) The method of claim 239, wherein said heterologous polypeptide is a secretory signal peptide.

241. (Previously presented) The polynucleotide of claim 240, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

242. (Previously presented) The method of claim 231, wherein said co-lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

243. (Previously presented) The method of claim 242, wherein said co-lipid is DPyPE.

244. (Previously presented) The method of claim 231, wherein said composition further comprises a nucleic acid molecule which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of: amino acids 30 to 764 of

SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8 and a combination of two or more of said amino acid sequences.

245. (Previously presented) A method to prevent anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof a composition comprising a carrier, (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE), a co-lipid and an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 97% identical to amino acids 30 to 764 of SEQ ID NO:4;

wherein said composition elicits an immune response to said polypeptide;

and wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

246. (Previously presented) The method of claim 245, wherein the amino acids of said polypeptide corresponding to amino acids 342 and 343 of SEQ ID NO:4 have been deleted.

247. (Previously presented) The method of claim 245, wherein said polypeptide comprises amino acids 199 to 764 of SEQ ID NO:4.

248. (Previously presented) The method of claim 245, wherein said nucleic acid fragment encodes a polypeptide at least 97% identical to amino acids 30 to 764 of SEQ ID NO:4.

249. (Previously presented) The method of claim 247, wherein said polypeptide comprises amino acids 30 to 764 of SEQ ID NO:4.

250. (Previously presented) The method of claim 248, wherein said the amino acids of said polypeptide corresponding to amino acids 192 to 197 of SEQ ID NO:4 have been deleted.

251. (Previously presented) The method of claim 250, wherein said polypeptide is SEQ ID NO:8.

252. (Previously presented) The method of claim 245, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

253. (Previously presented) The method of claim 252, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

254. (Previously presented) The method of claim 253, wherein said heterologous polypeptide is a secretory signal peptide.

255. (Previously presented) The method of claim 254, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

256. (Previously presented) The method of claim 245, wherein said co-lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

257. (Previously presented) The method of claim 256, wherein said co-lipid is 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE).

258. (Previously presented) The method of claim 257, wherein said DMRIE and DOPE are in a 1:1 molar ratio.

259. (Previously presented) The method of claim 258, wherein said polypeptide is SEQ ID NO:8.

260. (Previously presented) The method of claim 245, wherein said composition further comprises a nucleic acid molecule which encodes a polypeptide comprising an amino

acid sequence selected from the group consisting of: amino acids 30-764 of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8 and a combination of two or more of said amino acid sequences.

261. (Currently amended) A method to ~~treat~~ reduce the severity of anthrax infection in a vertebrate comprising: administering to a vertebrate in need thereof a composition comprising a carrier, (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE), a co-lipid and an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 97% identical to amino acids 30 to 764 of SEQ ID NO:4;

wherein said composition elicits an immune response to said polypeptide;

and wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

262. (Previously presented) The method of claim 261, wherein the amino acids of said polypeptide corresponding to amino acids 342 and 343 of SEQ ID NO:4 have been deleted.

263. (Previously presented) The method of claim 261, wherein said polypeptide comprises amino acids 199 to 764 of SEQ ID NO:4.

264. (Previously presented) The method of claim 261, wherein said nucleic acid fragment encodes a polypeptide at least 97% identical to amino acids 30 to 764 of SEQ ID NO:4.

265. (Previously presented) The method of claim 263, wherein said polypeptide comprises amino acids 30 to 764 of SEQ ID NO:4.

266. (Previously presented) The method of claim 264, wherein the amino acids of said polypeptide corresponding to amino acids 192 to 197 of SEQ ID NO:4 have been deleted.

267. (Previously presented) The method of claim 266, wherein said polypeptide is SEQ ID NO:8.

268. (Previously presented) The method of claim 261, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

269. (Previously presented) The method of claim 268, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

270. (Previously presented) The method of claim 269, wherein said heterologous polypeptide is a secretory signal peptide.

271. (Previously presented) The method of claim 270, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

272. (Previously presented) The method of claim 261, wherein said co-lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

273. (Previously presented) The method of claim 272, wherein said co-lipid is DPyPE.

274. (Previously presented) The method of claim 261, wherein said composition further comprises a nucleic acid molecule which encodes a polypeptide comprising an amino acid sequence selected from the group consisting of: amino acids 30 to 764 of SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8 and a combination of two or more of said amino acid sequences.

275. (Previously presented) A composition comprising a carrier, a lipid selected from the group consisting of: (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradecenyloxy)-1-propanaminium bromide (GAP-DMORIE), (±)-N-(2-hydroxyethyl)-

N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE) and a combination thereof, a co-lipid, and an isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 97% identical to amino acids 199 to 764 of SEQ ID NO:4,

wherein said composition elicits an immune response to said polypeptide;

and wherein said nucleic acid fragment is a variant fragment of an optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 11 of the 24 phenylalanine codons in said coding region are TTT and about 13 of said phenylalanine codons are TTC;

wherein about 5 of the 62 leucine codons in said coding region are TTA, about 8 of said leucine codons are TTG, about 8 of said leucine codons are CTT, about 12 of said leucine codons are CTC, about 4 of said leucine codons are CTA, and about 25 of said leucine codons are CTG;

wherein about 20 of the 57 isoleucine codons in said coding region are ATT, about 28 of said isoleucine codons are ATC, and about 9 of said isoleucine codons are ATA;

wherein the 10 methionine codons in said coding region are ATG;

wherein about 8 of the 43 valine codons in said coding region are GTT, about 10 of said valine codons are GTG, about 5 of said valine codons are GTA, and about 20 of said valine codons are GTG;

wherein about 13 of the 72 serine codons in said coding region are TCT, about 16 of said serine codons are TCC, about 11 of said serine codons are TCA, about 4 of said

serine codons are TCG, about 11 of said serine codons are AGT, and about 17 of said serine codons are AGC;

wherein about 8 of the 29 proline codons in said coding region are CCT, about 10 of said proline codons are CCC, about 8 of said proline codons are CCA, and about 3 of said proline codons are CCG;

wherein about 14 of the 58 threonine codons in said coding region are ACT, about 21 of said threonine codons are ACC, about 16 of said threonine codons are ACA, and about 7 of said threonine codons are ACG;

wherein about 11 of the 41 alanine codons in said coding region are GGT, about 17 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 12 of the 28 tyrosine codons in said coding region are TAT and about 16 of said tyrosine codons are TAC;

wherein about 4 of the 10 histidine codons in said coding region are CAT and about 6 of said histidine codons are CAC;

wherein about 8 of the 31 glutamine codons in said coding region are CAA and about 23 of said glutamine codons are CAG;

wherein about 32 of the 69 asparagine codons in said coding region are AAT and about 37 of said asparagine codons are AAC;

wherein about 25 of the 60 lysine codons in said coding region are AAA and about 35 of said lysine codons are AAG;

wherein about 22 of the 47 aspartic acid codons in said coding region are GAT and about 25 of said aspartic acid codons are GAC;

wherein about 21 of the 51 glutamic acid codons in said coding region are GAA and about 30 of said glutamic acid codons are GAG;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 2 of the 29 arginine codons in said coding region are CGT, about 6 of said arginine codons are CGC, about 3 of said arginine codons are CGA, about 6 of said arginine codons are CGG, about 6 of said arginine codons are AGA, and about 6 of said arginine codons are AGG; and

wherein about 6 of the 36 glycine codons in said coding region are GGT, about 12 of said glycine codons are GGC, about 9 of said glycine codons are GGA, and about 9 of said glycine codons are GGG.

276. (Previously presented) The composition of claim 275, wherein the amino acids of said polypeptide corresponding to amino acids 342 and 343 of SEQ ID NO:4 have been deleted.

277. (Previously presented) The composition of claim 275, wherein said polypeptide comprises amino acids 199 to 764 of SEQ ID NO:4.

278. (Previously presented) The composition of claim 275, wherein said nucleic acid fragment encodes a polypeptide at least 97% identical to amino acids 30 to 764 of SEQ ID NO:4.

279. (Previously presented) The composition of claim 277, wherein said polypeptide comprises amino acids 30 to 764 of SEQ ID NO:4.

280. (Previously presented) The composition of claim 278, wherein the amino acids of said polypeptide corresponding to amino acids 192 to 197 of SEQ ID NO:4 have been deleted.

281. (Previously presented) The composition of claim 280, wherein said polypeptide is SEQ ID NO:8.

282. (Previously presented) The composition of claim 275, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

283. (Previously presented) The composition of claim 282, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

284. (Previously presented) The composition of claim 283, wherein said heterologous polypeptide is a secretory signal peptide.

285. (Previously presented) The composition of claim 284, wherein said signal peptide is a human tissue plasminogen activator (hTPA) signal peptide.

286. (Previously presented) The composition of claim 275, wherein said co-lipid is selected from the group consisting of:

1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE),

1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and

1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

287. (Previously presented) The composition of claim 286, wherein said lipid is GAP-DMORIE.

288. (Previously presented) The composition of claim 286, wherein said lipid is DMRIE.

289. (Previously presented) The composition of claim 287, wherein said co-lipid is DPyPE.

290. (Previously presented) The composition of claim 288, wherein said co-lipid is DOPE.

291. (Previously presented) The composition of claim 289, wherein said polypeptide is SEQ ID NO:8.

292. (Previously presented) The composition of claim 290, wherein said polypeptide is SEQ ID NO:8.